

SEQUENCE LISTING

<110> Istituto Di Ricerche Di Biologia Molecolare P. Angeletti S.P.A.

<120> CARCINOEMBRYONIC ANTIGEN FUSIONS AND
USES THEREOF

<130> ITR0073Y PCT

<150> 60/635,791

<151> 2004-12-14

<150> 60/543,649

<151> 2004-02-11

<160> 54

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Artificial Sequence

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<223> PCR Primer

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31

<210> 2

<211> 35

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<213> Artificial Sequence

<220>

<223> PCR Primer

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<220>

<223> PCR Primer

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<210> 4

<211> 38

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<213> Artificial Sequence

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<400> 6
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<220>
<223> CEA-LTA fusion

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acgccgttca atgtcgaga ggggaaaggag gtgcTTCTAC ttgtccacaa tctgccccag 180
catctttttg gctacagctg gtacaaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata 300
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gatgctgtgg cttcacctg tgaacctgag actcaggacg caacctaccc ttgggtgggtt 540
aacaatcaga gcctcccggt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
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gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
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 gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggtg ggtaaataat 1080
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 gttgaccaca gcgacccagt catcctgaat gtcccttatg gcccagacga ccccaccatt 1260
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 aatgaggaga cccagaatct gagcacaata tatctcagga aatatacaatc aaaagttaag 2700
 aggcagatat ttccagacta tcagtcagag gttgacatataataacagaat tcgggatgaa 2760
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<210> 8

<211> 921

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 8

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Arg	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
	20							25					30		
Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly
	35							40					45		
Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly
	50							55					60		
Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
	65							70					75		80
Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser
	85							90					95		

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100 105 110
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210 215 220
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 290 295 300
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 325 330 335
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Leu Val Asn Gly Asp Lys Leu Tyr Arg
 675 680 685
 Ala Asp Ser Arg Pro Pro Asp Glu Ile Lys Arg Ser Gly Gly Leu Met
 690 695 700
 Pro Arg Gly His Asn Glu Tyr Phe Asp Arg Gly Thr Gln Met Asn Ile
 705 710 715 720
 Asn Leu Tyr Asp His Ala Arg Gly Thr Gln Thr Gly Phe Val Arg Tyr
 725 730 735
 Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser Leu Arg Ser Ala His Leu
 740 745 750
 Ala Gly Gln Ser Ile Leu Ser Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val
 755 760 765
 Ile Ala Thr Ala Pro Asn Met Phe Asn Val Asn Asp Val Leu Gly Val
 770 775 780
 Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu Gly Gly Ile
 785 790 795 800
 Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe Gly Val Ile
 805 810 815
 Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg
 820 825 830
 Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu Ala Gly Phe
 835 840 845
 Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile His His Ala
 850 855 860
 Pro Gln Gly Cys Gly Asn Ser Ser Arg Thr Ile Thr Asp Asp Thr Cys
 865 870 875 880
 Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg Lys Tyr Gln
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<210> 9
 <211> 2355
 <212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 9

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 tccccaaaaaa aagccattga aaggatggaa gacacattaa gaatcacata tctgaccgag 2280
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<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

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 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60
 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65 70 75 80
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100 105 110
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210 215 220
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 290 295 300
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 325 330 335
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 420 425 430

Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
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 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
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 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
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 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
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 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
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 610 615 620
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 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
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 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
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 675 680 685
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 690 695 700
 Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile
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 Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser
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 Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
 740 745 750
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 Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
 770 775 780

<210> 11
 <211> 2355
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEAopt-LTB fusion

<400> 11

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 cacCTGTTG gctacagCTG gtacaAGGGC gagcgcgtgg acggcaaccg ccagatcatc 240
 ggctacgtGA tcggCACCCa gcaggCCACC cccggccccG cctacAGCGG ccgcgagatc 300
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 accCTGcACG tgatCAAGAG cgacCTGGTg aacgaggAGG ccacGGCCA gttccgcgtG 420
 tACCCGAGC tgCCCAAGCC cagcatcAGC agcaacaACa gcaAGCCCGT ggaggacaAG 480
 gacGCCGTGG cCTTACACCTG cgagCCCGAG acccaggACG ccacCTACCT gtggTggGTG 540
 aacaaccAGA gcCTGCCCgt gaggCCCCGc ctgcAGCTGA gcaacGGCAA ccgcACCCtG 600
 accCTGTTCA acgtGACCCG caacGACACC gccAGCTACA agtgcgAGAC ccagaACCC 660
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 acccaggAGC tGTTcATCCC caacatcACC gtGAACAACA gCGGcAGCtA cacCTGCCAG 900
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 aacAGCGCCA gCGGCCACAG ccgcACCCACC gTGAAGAGCA tcACCGTgAG CGCCGAGCTG 1500
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 ctgCCCGTGA gCCCCCGCT gcAGCTGAGC aacGGCAACC gcACCCtGAC cCTGTTCAAC 1680
 gtgACCCGCA acgACGCCG cgcCTACGTG tgcGGCATCC agaACAGCGT gAGCGCCAAC 1740
 cgcAGCGACC ccgtGACCCt ggacGTGCTG tacGGCCCCG acACCCCCAT catCAGCCCC 1800
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 tTCATGCCA agATCACCCCC caacaACAC ggcACCTACG cCTGTTCTGT gagCAACCTG 1980
 gCCACCGGCC gCAACAAACAG catCgtGAAG agCATCACCG tgAGCGCCAG CGGCACCTCT 2040
 agAGCTCCCC agACTATTAC agAACTATGT tcggAAATATC gCAACACACA aATATATACG 2100
 atAAATGACA agATACTATC atATAcGGAA tcgatGGCAG gCAAAAGAGA aATGGTTATC 2160
 attACATTtA agAGCGGCCA aacATTtCAG gTCGAAGTCC cggcAGtCA acATATAGAC 2220
 tcccAGAAAA aAGCCATTGA aaggatGAAG gacACATTAA gaATCACATA tCTGACCGAG 2280
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<210> 12
 <211> 2358
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEAopt-LTBopt fusion

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 cacCTGTTG gctacagCTG gtacaAGGGC gagcgcgtgg acggcaaccg ccagatcatc 240
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 aacaaccaga gcctgcccgt gagccccccgc ctgcagctga gcaacggcaa ccgcaccctg 600
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<210> 13

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEAopt-LTBopt fusion

<400> 13

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				20				25				30			

Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly
				35				40			45				

Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly
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Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
65					70				75				80		

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
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 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
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 115 120 125
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 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
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 165 170 175
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 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
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 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
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 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
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 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
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 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
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 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Ile Thr Val Tyr Ala
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 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
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 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
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 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
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 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
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 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
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 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
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 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
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Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
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 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
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 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
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 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
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 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
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 Thr Val Ser Ala Ser Gly Thr Ser Arg Ala Pro Gln Ser Ile Thr Glu
 675 680 685
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 690 695 700
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 Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser
 725 730 735
 Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
 740 745 750
 Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val
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<210> 14
 <211> 2358
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> rhCEAopt-LTBopt fusion

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<210> 15

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEAopt-LTBopt fusion

<400> 15

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Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
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Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
65 70 75 80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
85 90 95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
100 105 110

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 Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180 185 190
 Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
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 Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
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 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
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 Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
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 Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
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 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
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Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
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 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
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 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
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 Ser Val Ser Ser Gly Asp Ser Ser Arg Ala Pro Gln Ser Ile Thr Glu
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 Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys
 690 695 700
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 705 710 715 720
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 Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
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 <211> 2118
 <212> DNA
 <213> Macaca mulatta

<400> 16

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 <212> DNA
 <213> Macaca mulatta

<400> 17

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 gtgaccttaa cctgtgaacc tgagactcag gacacaaccc acctgtggg ggtaaacaat 1080
 cagagcctct cggtcagttc caggctggag ctgtccaatg acaacaggac cctcaactgta 1140
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 gctaccggtc gcaataactc catagtcaag aacatcttag tctccctctgg cgattcagca 2040
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<210> 18
 <211> 705
 <212> PRT
 <213> Macaca mulatta

<400> 18

Met	Gly	Ser	Pro	Ser	Ala	Pro	Leu	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
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Thr	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
	20									25					30
Thr	Ala	Gln	Leu	Thr	Ile	Glu	Ser	Arg	Pro	Phe	Asn	Val	Ala	Glu	Gly
		35				40						45			
Lys	Glu	Val	Leu	Leu	Leu	Ala	His	Asn	Val	Ser	Gln	Asn	Leu	Phe	Gly
		50				55					60				
Tyr	Ile	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Ala	Ser	Arg	Arg	Ile	Gly
		65				70					75				80
Ser	Cys	Val	Ile	Arg	Thr	Gln	Gln	Ile	Thr	Pro	Gly	Pro	Ala	His	Ser
			85						90					95	
Gly	Arg	Glu	Thr	Ile	Asp	Phe	Asn	Ala	Ser	Leu	Leu	Ile	His	Asn	Val
		100				105						110			
Thr	Gln	Ser	Asp	Thr	Gly	Ser	Tyr	Thr	Ile	Gln	Val	Ile	Lys	Glu	Asp
		115				120					125				
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu
		130				135					140				
Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	Asp	Lys
	145				150					155				160	
Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Thr	Thr	Tyr
			165						170				175		
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Glu
			180					185					190		
Leu	Ser	Ser	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro	Arg	Asn
			195					200				205			
Asp	Thr	Thr	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Val	Arg
			210					215			220				
Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro
	225					230				235					240
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Pro	Tyr	Arg	Ala	Gly	Glu	Asn	Leu	Asn
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Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn
			275					280			285				
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Ala	Thr	Gly	Leu	Asn	Arg	Thr	Val	Thr	Ala	Ile	Thr	Val	Tyr	Ala	
	305					310				315				320	

Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
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 Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
 370 375 380
 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
 Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
 420 425 430
 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
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 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
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 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
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 Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
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 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
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 Arg Ala Thr Val Gly Ile Ile Gly Met Leu Val Gly Val Ala Leu
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 Met
 705

<210> 19
 <211> 705
 <212> PRT

<213> Macaca mulatta

<400> 19

Met	Gly	Ser	Pro	Ser	Ala	Pro	Leu	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
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									20	25				30	
Thr	Ala	Gln	Leu	Thr	Ile	Glu	Ser	Arg	Pro	Phe	Asn	Val	Ala	Glu	Gly
								35	40				45		
Lys	Glu	Val	Leu	Leu	Leu	Ala	His	Asn	Val	Ser	Gln	Asn	Leu	Phe	Gly
								50	55				60		
Tyr	Ile	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Ala	Ser	Arg	Arg	Ile	Gly
65								70			75			80	
Ser	Cys	Val	Ile	Arg	Thr	Gln	Gln	Ile	Thr	Pro	Gly	Pro	Ala	His	Ser
								85			90			95	
Gly	Arg	Glu	Thr	Ile	Asp	Phe	Asn	Ala	Ser	Leu	Leu	Ile	His	Asn	Val
								100			105			110	
Thr	Gln	Ser	Asp	Thr	Gly	Ser	Tyr	Thr	Ile	Gln	Val	Ile	Lys	Glu	Asp
								115			120			125	
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu
								130			135			140	
Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	Asp	Lys
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Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Thr	Thr	Tyr
								165			170			175	
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								180			185			190	
Leu	Ser	Ser	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro	Arg	Asn
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								210			215			220	
Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro
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Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn
								275			280			285	
Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Met	Cys	Gln	Ala	His	Asn	Ser
								290			295			300	
Ala	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Ala	Ile	Thr	Val	Tyr	Ala
305								310						320	
Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Ile	Glu
								325			330			335	
Asp	Lys	Asp	Ala	Val	Thr	Leu	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Thr
								340			345			350	
Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser	Ser	Arg
								355			360			365	
Leu	Glu	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro
								370			375			380	
Arg	Asn	Asp	Thr	Thr	Phe	Tyr	Glu	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser
385								390						400	
Val	Arg	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp
								405			410			415	

Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
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 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Phe
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
 450 455 460
 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
 500 505 510
 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Asn Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
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 675 680 685
 Arg Ala Thr Val Gly Ile Ile Gly Met Leu Val Gly Val Ala Leu
 690 695 700
 Met
 705

<210> 20
 <211> 702
 <212> PRT
 <213> Homo sapiens

<400> 20
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 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65 70 75 80
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100 105 110
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210 215 220
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 290 295 300
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Ile Thr Val Tyr Ala
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 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 325 330 335
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
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 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
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 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
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<210> 21
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEAoptDOMopt fusion

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<210> 22
 <211> 2037
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> deleted human CEA

<400> 22

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gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
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<400> 23

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Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
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 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
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 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
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 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
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 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
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 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
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 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
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 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
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 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
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 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
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Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
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 <213> Artificial Sequence

<220>
 <223> CEA-FRC fusion

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<211> 2664

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-FcIgG fusion

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<211> 2167

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LAMP fusion

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<211> 3921

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-HSP70 fusion

<400> 27

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEA-VSVG fusion

<400> 28

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<210> 29
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
<223> PCR primer

<400> 29
tattctagat tcaacaccaa ttccattttc ttattc 36

<210> 30
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 30
gcggccgcta gaatcatttg tccatccttc atc 33

<210> 31
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 31
tattctagat tcaacaccaa ttccattttc ttattc 36

<210> 32
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 32
tttagccggccg ctagttctgt atcatatcgt aaaggg 36

<210> 33
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 33
tctagataaa actcacacat gcccc 25

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 34
gccgactcat ttacccggag acagggag 28

<210> 35
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 35
tctagatttg atccccattg ctgtgggcgg tgccctg 37

<210> 36
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 36
ggcgtgactc ctcttcctgc caatgaggta ggcaatgag 39

<210> 37
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 37
atatcttagat ttcaccatag tttttccaca caacc 35

<210> 38
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 38
gcggccgcct tccttccaag tcggttcatc tctatg 36

<210> 39
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 39
gctctagata tggctcgtgc ggtcgggatc gacc 34

<210> 40
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 40
gccgcggccg ctcacttggc ctcccgccg tcgtcg 36

<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 41
gttatctaga agcaccccca tccc 24

<210> 42
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 42
ttaagatctc taagatctgg tgtcgtatct cagggg 36

<210> 43
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 43
ttatctagaa agacccacac ctgccccct tgc 33

<210> 44
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 44
tatagatctt agggcacctt acttgccggg g

31

<210> 45
<211> 952
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA-Dom fusion

<400> 45
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Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
35 40 45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
100 105 110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
115 120 125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
130 135 140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145 150 155 160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
165 170 175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
180 185 190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
195 200 205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
210 215 220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225 230 235 240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
245 250 255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
260 265 270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
275 280 285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
290 295 300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305 310 315 320

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 325 330 335
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Ser Arg Ser Thr Pro Ile Pro Phe Ser
 675 680 685
 Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp
 690 695 700
 Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp
 705 710 715 720
 Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro
 725 730 735
 Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val
 740 745 750

Asn	Asn	Glu	Ser	Ser	Glu	Val	Ile	Val	His	Lys	Ala	Met	Asp	Ile	Glu
755					760							765			
Tyr	Asn	Asp	Met	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val
770					775							780			
Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Gln	Tyr	Gly	Thr	Asn	Glu	Tyr
785					790					795			800		
Ser	Ile	Ile	Ser	Ser	Met	Lys	Lys	His	Ser	Leu	Ser	Ile	Gly	Ser	Gly
					805				810			815			
Trp	Ser	Val	Ser	Leu	Lys	Gly	Asn	Asn	Leu	Ile	Trp	Thr	Leu	Lys	Asp
					820				825			830			
Ser	Ala	Gly	Glu	Val	Arg	Gln	Ile	Thr	Phe	Arg	Asp	Leu	Pro	Asp	Lys
					835			840			845				
Phe	Asn	Ala	Tyr	Leu	Ala	Asn	Lys	Trp	Val	Phe	Ile	Thr	Ile	Thr	Asn
					850			855			860				
Asp	Arg	Leu	Ser	Ser	Ala	Asn	Leu	Tyr	Ile	Asn	Gly	Val	Leu	Met	Gly
865					870				875			880			
Ser	Ala	Glu	Ile	Thr	Gly	Leu	Gly	Ala	Ile	Arg	Glu	Asp	Asn	Asn	Ile
					885			890			895				
Thr	Leu	Lys	Leu	Asp	Arg	Cys	Asn	Asn	Asn	Gln	Tyr	Val	Ser	Ile	
					900			905			910				
Asp	Lys	Phe	Arg	Ile	Phe	Cys	Lys	Ala	Leu	Asn	Pro	Lys	Glu	Ile	Glu
					915			920			925				
Lys	Leu	Tyr	Thr	Ser	Tyr	Leu	Ser	Ile	Thr	Phe	Leu	Arg	Asp	Phe	Trp
					930			935			940				
Gly	Asn	Pro	Leu	Arg	Tyr	Asp	Thr								
					945			950							

<210> 46

<211> 907

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-FcIgG fusion

<400> 46

Met	Glu	Ser	Pro	Ser	Ala	Pro	Pro	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
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Arg	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
					20			25				30			
Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly
					35			40				45			
Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly
					50			55			60				
Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
					65			70			75			80	
Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser
					85			90				95			
Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile
					100			105				110			
Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp
					115			120			125				

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210 215 220
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 290 295 300
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 325 330 335
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560

Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Ser Arg Lys Thr His Thr Cys Pro Pro
 675 680 685
 Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 690 695 700
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 705 710 715 720
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 725 730 735
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 740 745 750
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 755 760 765
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 770 775 780
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 785 790 795 800
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 805 810 815
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 820 825 830
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 835 840 845
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 850 855 860
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 865 870 875 880
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 885 890 895
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 900 905

<210> 47
 <211> 825
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DOM

<400> 47

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 attatatcag atatatctgg gtttaattca tctgtataa catatccaga tgctcaattg 180
 gtgcccggaa taaatggcaa agcaatacat tttagtaaaca atgaatcttc tgaagttata 240
 gtgcataaag ctatggatata tgaatataat gatatgttta ataattttac cgtagctt 300
 tggttgaggg ttccctaaagt atctgctagt catttagaac aatatggcac aaatgagtt 360
 tcaataataa gctctatgaa aaaacatagt ctatcaatag gatctggttg gagtgatca 420
 cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 480
 acttttaggg atttacctga taaatttaat gcttatttag caaataaaatg ggttttata 540
 actattacta atgatagatt atcttctgct aatttgtata taaatggagt acttatggga 600
 agtgcagaaa ttactggttt aggagctatt agagaggata ataatataac attaaaacta 660
 gatagatgtata ataataataa tcaatacggtt tctattgata aatttaggtt attttgcaaa 720
 gcattaaatc caaaagagat tgaaaaattt tacacaagtt atttatctat aacctttta 780
 agagacttct ggggaaaccc ttacgatata gatacagata ggttag 825

<210> 48

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> DOM

<400> 48

Asp	Ser	Thr	Pro	Ile	Pro	Phe	Ser	Tyr	Ser	Lys	Asn	Leu	Asp	Cys	Trp
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Val	Asp	Asn	Glu	Glu	Asp	Ile	Asp	Val	Ile	Leu	Lys	Lys	Ser	Thr	Ile
	20														30
Leu	Asn	Leu	Asp	Ile	Asn	Asn	Asp	Ile	Ile	Ser	Asp	Ile	Ser	Gly	Phe
		35													45
Asn	Ser	Ser	Val	Ile	Thr	Tyr	Pro	Asp	Ala	Gln	Leu	Val	Pro	Gly	Ile
			50												60
Asn	Gly	Lys	Ala	Ile	His	Leu	Val	Asn	Glu	Ser	Ser	Glu	Val	Ile	
	65														80
Val	His	Lys	Ala	Met	Asp	Ile	Glu	Tyr	Asn	Asp	Met	Phe	Asn	Asn	Phe
				85											95
Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu
															100
															105
Glu	Gln	Tyr	Gly	Thr	Asn	Glu	Tyr	Ser	Ile	Ile	Ser	Ser	Met	Lys	Lys
		115													125
His	Ser	Leu	Ser	Ile	Gly	Ser	Gly	Trp	Ser	Val	Ser	Leu	Lys	Gly	Asn
	130														140
Asn	Leu	Ile	Trp	Thr	Leu	Lys	Asp	Ser	Ala	Gly	Glu	Val	Arg	Gln	Ile
		145													160
Thr	Phe	Arg	Asp	Leu	Pro	Asp	Lys	Phe	Asn	Ala	Tyr	Leu	Ala	Asn	Lys
				165											175
Trp	Val	Phe	Ile	Thr	Ile	Thr	Asn	Asp	Arg	Leu	Ser	Ser	Ala	Asn	Leu
															180
															185
Tyr	Ile	Asn	Gly	Val	Leu	Met	Gly	Ser	Ala	Glu	Ile	Thr	Gly	Leu	Gly
		195													205
Ala	Ile	Arg	Glu	Asp	Asn	Asn	Ile	Thr	Leu	Lys	Leu	Asp	Arg	Cys	Asn
		210													220
Asn	Asn	Asn	Gln	Tyr	Val	Ser	Ile	Asp	Lys	Phe	Arg	Ile	Phe	Cys	Lys
	225														240

Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser
 245 250 255
 Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
 260 265 270
 Asp Arg

<210> 49
 <211> 2857
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> CEA-DOM fusion

<400> 49
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 acggccgttca atgtcgcaga ggggaaggag gtgtttctac ttgtccacaa tctgccccag 180
 catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
 ggatatgtaa taggaactca acaagctacc ccaggccccg catacagtgg tcgagagata 300
 atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
 accctacacg tcataaaagtc agatcttgc aatgaagaag caactggcca gttccgggta 420
 taccggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccctg ggaggacaag 480
 gatgctgtgg cttcacctg tgaacctgag actcaggacg caacctacct gtgggtggta 540
 aacaatcaga gcctcccggt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
 actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccac 660
 gtgagtgcca ggcgcagtga ttcaagtcatc ctgaatgtcc tctatggccc gatgcccc 720
 accatttccc ctctaaaacac atcttacaga tcagggaaa atctgaacct ctcctgcccac 780
 gcagcctcta acccacctgc acagtaactt tggtttgc aatggacttt ccagcaatcc 840
 acccaagagc tcttattccc caacatcaact gtgaataata gtggatccta tacgtgccaa 900
 gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
 gagccaccca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020
 gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggtg gtaaataat 1080
 cagagcctcc cggtcagtcc caggctgcag ctgtccatg acaacaggac cctcactcta 1140
 ctcagtgtca caaggaatga tgttaggaccc tatgagtgtg gaatccagaa cgaattaatg 1200
 gttgaccaca ggcgacccagt catcctgaat gtcctctatg gcccagacga ccccaccatt 1260
 tccccctcat acaccttata ccgtccagggt gtgaacctca gcctctcctg ccatgcagcc 1320
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 gagcttttca tctccaacat cactgagaag aacagcggac tctataccctg ccaggccaaat 1440
 aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgcggagctg 1500
 cccaaaggccct ccatctccag caacaactcc aaacccgtgg aggacaagga tgctgtggcc 1560
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 ctcccagtca gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680
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 ccagactcgt cttaccttcc gggagcgaac ctcacacctct cctgccactc ggcctcta 1860
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 tcaataatata gctctatgaa aaaacatagt ctatcaatag gatctggttg gagtgatca 2460
 cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 2520
 acttttaggg atttacctga taaatttaat gcttatttag caaataaaatg ggttttata 2580
 actattacta atgatagatt atcttctgct aatttgtata taaatggagt acttattggga 2640
 agtgcagaaa ttactggttt aggagctatt agagaggata ataataaaac attaaaacta 2700
 gatagatgtt ataataataa tcaatacgtt tctattgata aatttaggtt atttgcaaa 2760
 gcattaaatc caaaagagat tgaaaaattt tacacaagtt atttatctat aacctttta 2820
 agagacttct gggaaaaccc ttacgatata gatata 2857

<210> 50

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 50

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 accggccagcc tgctgacattt ctggaaaccccc cccaccaccc cccagctgac catcgagagc 120
 cgcccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
 aacctgttgc gctacatctg gtacaaggagc gagcgcgtgg acgcccagccg ccgcattcggc 240
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 taccggcagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccggt ggaggacaag 480
 gacggcgtgg ccctgacctg cgagcccgag acccaggaca ccacccatct gtggtgggtg 540
 aacaaccaga gcctgcccgt gagcccccgc ctggagctga gcagcgacaa ccgcacccctg 600
 accgtgttca acatccccccg caacgcacacc accagctaca agtgcgagac ccagaacccc 660
 gtgagcgtgc gccgcagcga cccctgtgacc ctgaacgtgc tgtacggccc cgacgcccc 720
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 gcccgcagca accccaccgc ccagtaatcc tggttcgtga acggcacctt ccagcagagc 840
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 cccgacccctga gctacccgcac ccgcgcaccc ctgaacccctga gctgcccacag cgacccac 1860
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agaaggcaccc ccatcccatt cagctacagc aagaacctgg actgctgggt ggacacaacgag 2100
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 gtgcacaagg ccatggacat cgagtacaac gacatgttca acaacttcac cgtgagctc 2340
 tggctgagag tgcctaaggat gagcgccagc caccctggagc agtacggcac caacgagttac 2400
 agcatcatca gcagcatgaa gaagcacagc ctgagcatcg gcagcggctg gagcgtgagc 2460
 ctgaaggcga acaacctcat ctggaccctg aaggatagcg ccggagaggt gagacagatc 2520
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 accatcacca acgacagact gagcagcgcc aacctgtaca tcaacggcgt gctcatggc 2640
 agcggcgaga tcaccggct gggcgccatc agagaggaca acaacatcac cctgaagctg 2700
 gacagatgca acaacaacaa ccagtacgtg agcatcgaca agttccggat cttctgcaag 2760
 gccctgaacc ccaaggagat cgagaagctg tacaccagct acctgagcat cacccctg 2820
 agagacttct gggcaaccc cctgagatac gacacctag 2859

<210> 51
 <211> 952
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> rhCEA-DOMopt fusion

<400> 51
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 Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
 50 55 60
 Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
 65 70 75 80
 Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
 85 90 95
 Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
 100 105 110
 Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180 185 190
 Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
 195 200 205
 Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240

Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
 245 250 255
 Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
 290 295 300
 Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
 325 330 335
 Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
 370 375 380
 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
 Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
 420 425 430
 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
 450 455 460
 Pro Asn Ile Thr Val Asn Asn Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
 500 505 510
 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670

Ser Val Ser Ser Gly Asp Ser Ser Arg Ser Thr Pro Ile Pro Phe Ser
 675 680 685
 Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp
 690 695 700
 Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp
 705 710 715 720
 Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro
 725 730 735
 Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val
 740 745 750
 Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu
 755 760 765
 Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
 770 775 780
 Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr
 785 790 795 800
 Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly
 805 810 815
 Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp
 820 825 830
 Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys
 835 840 845
 Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn
 850 855 860
 Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly
 865 870 875 880
 Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile
 885 890 895
 Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile
 900 905 910
 Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu
 915 920 925
 Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp
 930 935 940
 Gly Asn Pro Leu Arg Tyr Asp Thr
 945 950

<210> 52
 <211> 2359
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> rhCEA-CTB opt fusion

<400> 52
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 cggcccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
 aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg cccgcacatcgcc 240
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 taccggcagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccggt ggaggacaag 480

gacgcccgtgg ccctgacctg cgagccccgag acccaggaca ccacctacct gtgggtgggtg 540
 aacaaccaga gcctgcccgt gagcccccgcttggagctga gcagcgacaa ccgcaccctg 600
 accgtgttca acatcccccg caacgacacc accagctaca agtgcgagac ccagaacccc 660
 gtgagcgtgc gccgcagcga ccccggtgacc ctgaacgtgc tgtacggccc cgacgcccc 720
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 ttcaacatcc cccgcaacga caccacccctc tacgagtgcg agaccaggaa ccccggtgagc 1200
 gtgcgcccgc gcgaccggcgttggacc gacaccacct acctgtggtg ggtgaacaac 1260
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 cccgacactga gctaccgcag ccgcgcacccctgac gctgcacag cgacagcaac 1860
 cccagccccc agtacagctg gctgatcaac ggacccctgc gccagcacac ccaggtgctg 1920
 ttcatcagca agatcaccag caacaacagc ggccgcctacg cctgcttgcgt gagaacactg 1980
 gccaccggcc gcaacaacag catcgtgaag aacatcagcg tgagcagcgg cgacagctct 2040
 agaacccttc agaacatcac cgatctgtgc gccgagtacc acaacaccca gatctacacc 2100
 ctgaacgaca agatcttcag ctacaccgg agcctggccg gcaagagaga gatggccatc 2160
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 agccagaaga aggccatcga gcgatgaaag gacaccctgc ggatgcctta cctcaccgag 2280
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<210> 53

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEA-CTBopt fusion

<400> 53

Met	Gly	Ser	Pro	Ser	Ala	Pro	Leu	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
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Thr	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
															20
															25
															30
Thr	Ala	Gln	Leu	Thr	Ile	Glu	Ser	Arg	Pro	Phe	Asn	Val	Ala	Glu	Gly
															35
															40
															45
Lys	Glu	Val	Leu	Leu	Leu	Ala	His	Asn	Val	Ser	Gln	Asn	Leu	Phe	Gly
															50
															55
															60
Tyr	Ile	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Ala	Ser	Arg	Arg	Ile	Gly
															65
															70
															75
															80
Ser	Cys	Val	Ile	Arg	Thr	Gln	Gln	Ile	Thr	Pro	Gly	Pro	Ala	His	Ser
															85
															90
															95

Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
 100 105 110
 Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180 185 190
 Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
 195 200 205
 Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
 245 250 255
 Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
 290 295 300
 Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
 325 330 335
 Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
 370 375 380
 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
 Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
 420 425 430
 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
 450 455 460
 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
 500 505 510
 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
 515 520 525

Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
 Ser Val Ser Ser Gly Asp Ser Ser Arg Thr Pro Gln Asn Ile Thr Asp
 675 680 685
 Leu Cys Ala Glu Tyr His Asn Thr Gln Ile Tyr Thr Leu Asn Asp Lys
 690 695 700
 Ile Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile
 705 710 715 720
 Ile Thr Phe Lys Asn Gly Ala Ile Phe Gln Val Glu Val Pro Gly Ser
 725 730 735
 Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
 740 745 750
 Leu Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val
 755 760 765
 Trp Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 770 775 780

<210> 54
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> tetanus toxoid peptide

<400> 54
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 Ser His Leu Glu
 20